Amendments to the claims:

Please amend the claims as shown below:

1. (Currently Amended) A composition comprising a substantially purified AviIII peptide, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme having at least 70% identity to SEQ ID NO. 3 1 and a carbohydrate binding domain (CBD) III, the catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII_Aace):

```
GH74_Ace        ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII_Aac      AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
                *::*.***.**. **** *. ***** .* *: *.****** ** :: :  * **:****

GH74_Ace        WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG
AviIII_Aac      NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPFKVG
                 :.*   *: ::*:**::*::*:.*******.**** *:****:*** **  * ****:*

GH74_Ace        GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD
AviIII_Aac      QNMPGRGMGERLAVDPNKNSILYFGARSGHGLWKSTDYGATWSNVTSFTWTGTYFQDSSS
                r*****************::.****** **:***:*** *****::*.*. .***: :.:.

GH74_Ace        TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAP-T
AviIII_Aac      T--YTSDPVGIAWVTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY
                *  * **  *:.**:**.:*.* *.*:  *******..:.** *.*.**** *.* *

GH74_Ace        GFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYF
AviIII_Aac      GFLPHKGVLSPEEXTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISP---TSLASTYY
                **:*****:.* ::.***: :* .*****:.* * *:.:***.** ***   *. *. *:

GH74_Ace        GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDIS
AviIII_Aac      GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDSGATWSPIWEWNGYPSINYYYSYDIS
                **.**::* * *.*:***:  .**** :****** ****: **:*..**. .  *  ***

GH74_Ace        AEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AviIII_Aac      NAPWIQDTTSTDQFP--VRVGWMVEALAIDPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV
                  **:   ...:       ::*** **:*****:*:: ***** *:*. :***:***  ::

GH74_Ace        HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIPTSPVPTTGTSV
AviIII_Aac      TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI
                 : .:. *:** ** .**:**.*..*:**:** *** *:*: *.*.  : :*.: * ..:

GH74_Ace        DYAELNPSIIVRAGSFDPSSQFNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR
AviIII_Aac      DYAGNKPSNIVRSGASDDYP-----TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT
                *** :** ***:*: *  .      :*:*:: *..*: .  ..  *  *:** ****.


GH74_Ace        FVWAPGDPGQPVVYAVGFGNSWAASQGVPANAQIRSDRVNPKTFYALSNGTFYRSTDGGV
AviIII_Aac      VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT
                .:  .. .*  *  : *   : :* ..:*:.* * **: : ..**. * *::* *.: ..

GH74_Ace        TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII_Aac      SPTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF
                :*  ..: * ** :*..:  * *.  **:* ::..**:***: **::: * :**::. ..

GH74_Ace        GFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
```

```
AviIII_Aac      GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT
                ****::. .** .:: . **.*.:* ::*:*.**.* :*.* .* :*.  .:.:.** .

GH74_Ace        LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac      YGRVFRGKERPGHLLRQSQRRPAG
                  **: * :  * :  :    *:* .
```

2. (Previously Amended) The composition of claim 1 wherein the AviIII peptide is further defined as comprising a linker and a signal sequence.

3. (Previously Cancelled)

4. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.

5. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 90 amino acids.

6. (Previously Amended) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.

7. (Currently Amended) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the ~~a~~ polypeptide sequence of SEQ ID NO: 4.

8. (Previously Amended) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Previously Amended) The composition of claim 1 wherein said AviIII protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Currently Amended) The composition of claim 1, wherein the catalytic domain of GH74_Ace ~~including~~ has at least 90% sequence identity with SEQ ID NO: 3.

11. (Currently Amended) The composition of claim 1, wherein the catalytic domain of GH74 ~~including~~ has at least 80% sequence identity ~~to~~ with SEQ ID NO: 3.

12. (Previously Amended) An isolated AviIII peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Previously Amended) An industrial mixture suitable for degrading cellulose, such mixture comprising the AviIII polypeptide of claim 1.

15. (Original) The industrial mixture of claim 14 further defined as comprising a detergent..

16-27 (Cancelled)

28. (Previously Amended) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

a) a polypeptide sequence of SEQ ID NO: 3;

b) a polypeptide sequence of SEQ ID NO: 4;

c) a polypeptide sequence of SEQ ID NO: 5;

d) a polypeptide sequence of SEQ ID NO: 1; and

e) combinations thereof.

29. (Previously Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Amended) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemaglutinin, glutathione S-tranferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)